

Re-run

HJ

PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,035

DATE: 08/31/2001

TIME: 11:38:07

Input Set : A:\227274078.ST25.txt

Output Set: N:\CRF3\08312001\I674035.raw

3 <110> APPLICANT: Lang, Jas  
 5 <120> TITLE OF INVENTION: Detecting the Expression of the DESC1 Gene in Squamous Cell Carcinoma

7 <130> FILE REFERENCE: 22727/04078  
 9 <140> CURRENT APPLICATION NUMBER: 09/674,035  
 10 <141> CURRENT FILING DATE: 1999-11-11  
 12 <150> PRIOR APPLICATION NUMBER: PCT/IB99/01818  
 13 <151> PRIOR FILING DATE: 1999-11-11  
 15 <160> NUMBER OF SEQ ID NOS: 10  
 17 <170> SOFTWARE: PatentIn version 3.0  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 1269  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Homo sapiens  
 24 <220> FEATURE:  
 25 <221> NAME/KEY: CDS  
 26 <222> LOCATION: (1)..(1269)  
 28 <400> SEQUENCE: 1

ENTERED

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31 1 5 10 15	
33 ccc tgg gtt atc ggc ctc gtc atc ttc ata tcc ctg att gtc ctg gca	96
34 Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile Val Leu Ala	
35 20 25 30	
37 gtg tgc att gga ctc act gtt cat tat gtg aga tat aat caa aag aag	144
38 Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys	
39 35 40 45	
41 acc tac aat tac tat agc aca ttg tca ttt aca act gac aaa cta tat	192
42 Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr	
43 50 55 60	
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46 Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln	
47 65 70 75 80	
49 aga ctt gaa tca atg gtg aaa aat gca ttt tat aaa tct cca tta agg	288
50 Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg	
51 85 90 95	
53 gaa gaa ttt gtc aag tct cag gtt atc aag ttc agt caa gac aag cat	336
54 Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Asp Lys His	
55 100 105 110	
57 gga gtg ttg gct cat atg ctg ttg att tgt aga ttt cac tct act gag	384
58 Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu	
59 115 120 125	
61 gat cct gaa act gta gat aaa att gtt caa ctt gtt tta cat gaa aag	432
62 Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys	
63 130 135 140	
65 ctg caa gat gct gta gga ccc cct aaa gta gat cct cac tca gtt aaa	480
66 Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys	
67 145 150 155 160	

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69	att aaa aaa atc aac aag aca gaa aca gac agc tat cta aac cat tgc	528
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71	165 170 175	
73	tgc gga aca cga aga agt aaa act cta ggt cag agt ctc agg atc gtt	576
74	Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val	
75	180 185 190	
77	ggt ggg aca gaa gta gaa gag ggt gaa tgg ccc tgg cag gct agc ctg	624
78	Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu	
79	195 200 205	
81	cag tgg gat ggg agt cat gcg tgt gga gca acc tta att aat gcc aca	672
82	Gln Trp Asp Gly Ser His Ala Cys Gly Ala Thr Leu Ile Asn Ala Thr	
83	210 215 220	
85	tgg ctt gtg agt gct gct cac tgt ttt aca aca tat aag aac cct gcc	720
86	Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala	
87	225 230 235 240	
89	aga tgg act gct tcc ttt gga gta aca ata aaa cct tcg aaa atg aaa	768
90	Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys	
91	245 250 255	
93	cgg ggt ctc cgg aga ata att gtc cat gaa aaa tac aaa cac cca tca	816
94	Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser	
95	260 265 270	
97	cat gac tat gat att tct ctt gca gag ctt tct agc cct gtt ccc tac	864
98	His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr	
99	275 280 285	
101	aca aat gca gta cat aga gtt tgt ctc cct gat gca tcc tat gag ttt	912
102	Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe	
103	290 295 300	
105	caa cca ggt gat gtg atg ttt gtg aca gga ttt gga gca ctg aaa aat	960
106	Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn	
107	305 310 315 320	
109	gat ggt tac agt caa aat cat ctt cga caa gca cag gtg act ctc ata	1008
110	Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile	
111	325 330 335	
113	gac gct aca act tgc aat gaa cct caa gct tac aat gac gcc ata act	1056
114	Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr	
115	340 345 350	
117	cct aga atc tta tgt gct ggc tcc tta gaa gga aaa aca gat gca tgc	1104
118	Pro Arg Ile Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys	
119	355 360 365	
121	cag ggt gac tct gga gga cca ctg gtt agt tca gat gct aga gat atc	1152
122	Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile	
123	370 375 380	
125	tgg tac ctt gct gga ata gtg agc tgg gga gat gaa tgt gcg aaa ccc	1200
126	Trp Tyr Leu Ala Gly Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro	
127	385 390 395 400	
129	aac aag cct ggt gtt tat act aga gtt acg gcc ttg cgg gac tgg att	1248
130	Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile	
131	405 410 415	
133	act tca aaa act ggt atc taa	1269

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138 <210> SEQ ID NO: 2
139 <211> LENGTH: 422
140 <212> TYPE: PRT
141 <213> ORGANISM: Homo sapiens
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150                               20                               25                               30
153 Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys
154                               35                               40                               45
157 Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr
158                               50                               55                               60
161 Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln
162 65                               70                               75                               80
165 Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg
166                               85                               90                               95
169 Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Asp Lys His
170                               100                              105                              110
173 Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu
174                               115                              120                              125
177 Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys
178                               130                              135                              140
181 Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys
182 145                              150                              155                              160
185 Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys
186                               165                               170                               175
189 Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val
190                               180                               185                               190
193 Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
194                               195                               200                               205
197 Gln Trp Asp Gly Ser His Ala Cys Gly Ala Thr Leu Ile Asn Ala Thr
198                               210                               215                               220
201 Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala
202 225                              230                              235                              240
205 Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys
206                               245                               250                               255
209 Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser
210                               260                               265                               270
213 His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr
214                               275                               280                               285
217 Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe
218                               290                               295                               300
221 Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn
222 305                              310                              315                              320
225 Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile
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229 Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr
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233 Pro Arg Ile Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys
234          355          360          365
237 Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile
238          370          375          380
241 Trp Tyr Leu Ala Gly Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro
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253 <210> SEQ ID NO: 3
254 <211> LENGTH: 1269
255 <212> TYPE: DNA
256 <213> ORGANISM: Homo sapiens
258 <220> FEATURE:
259 <221> NAME/KEY: CDS
260 <222> LOCATION: (1)..(1269)
262 <400> SEQUENCE: 3
263 atg tat cgg cca gat gtg gtg agg gct agg aaa aga gtt tgt tgg gaa      48
264 Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys Trp Glu
265 1          5          10          15
267 ccc tgg gtt atc ggc ctc gtc atg ttc ata tcc ctg att gtc ctg gca      96
268 Pro Trp Val Ile Gly Leu Val Met Phe Ile Ser Leu Ile Val Leu Ala
269          20          25          30
271 gtg tgc att gga gtc act gtt cat tat gtg aga tat aat caa aag aag      144
272 Val Cys Ile Gly Val Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys
273          35          40          45
275 acc tac aat tac tat agc aca ttg tca ttt aca act gac aaa cta tat      192
276 Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr
277          50          55          60
279 gct gag ttt ggc aga gag gct tct aac aat ttt aca gaa atg agc cag      240
280 Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln
281 65          70          75          80
283 aga ctt gaa tca atg gtg aaa aat gca ttt tat aaa tct cca tta agg      288
284 Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg
285          85          90          95
287 gaa gaa ttt gtc aag tct cag gtt atc aag ttc agt caa cag aag cat      336
288 Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His
289          100          105          110
291 gga gtg ttg gct cat atg ctg ttg att tct aga ttt cac tct act gag      384
292 Gly Val Leu Ala His Met Leu Leu Ile Ser Arg Phe His Ser Thr Glu
293          115          120          125
295 gat cct gaa act gta gat aaa att gtt caa ctt gtt tta cat gaa aag      432
296 Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys
297          130          135          140
299 ctg caa gat gct gta gga ccc cct aaa gta gat cct cac tca gtt aaa      480
300 Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys

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301	145		150		155		160	
303	att	aaa	aaa	atc	aac	aag	aca	gaa
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307	tgc	gga	aca	cga	aga	agt	aaa	act
308	Cys	Gly	Thr	Arg	Arg	Ser	Lys	Thr
309				180				185
311	ggt	ggg	aca	gaa	gta	gaa	gag	ggt
312	Gly	Gly	Thr	Glu	Val	Glu	Glu	Gly
313			195					200
315	cag	tgg	gat	ggg	agt	cat	cgc	tgt
316	Gln	Trp	Asp	Gly	Ser	His	Arg	Cys
317		210				215		220
319	tgg	ctt	gtg	agt	gct	gct	cac	tgt
320	Trp	Leu	Val	Ser	Ala	Ala	His	Cys
321	225				230			235
323	aga	tgg	act	gct	tcc	ttt	gga	gta
324	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val
325				245				250
327	cgg	ggt	ctc	cgg	aga	ata	att	gtc
328	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val
329				260				265
331	cat	gac	tat	gat	att	tct	ctt	gca
332	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala
333		275				280		285
335	aca	aat	gca	gta	cat	aga	gtt	tgt
336	Thr	Asn	Ala	Val	His	Arg	Val	Cys
337		290				295		300
339	caa	cca	ggt	gat	gtg	atg	ttt	gtg
340	Gln	Pro	Gly	Asp	Val	Met	Phe	Val
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343	gat	ggt	tac	agt	caa	aat	cat	ctt
344	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu
345				325				330
347	gac	gct	aca	act	tgc	aat	gaa	cct
348	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro
349			340					345
351	cct	aga	atg	tta	tgt	gct	ggc	tcc
352	Pro	Arg	Met	Leu	Cys	Ala	Gly	Ser
353			355					360
355	cag	ggt	gac	tct	gga	gga	cca	ctg
356	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu
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364	Asn	Lys	Pro	Gly	Val	Tyr	Thr	Arg
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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/674,035

DATE: 08/31/2001

TIME: 11:38:09

Input Set : A:\227274078.ST25.txt

Output Set: N:\CRF3\08312001\I674035.raw

**STATISTICS SUMMARY**

PATENT APPLICATION: US/09/674,035

DATE: 08/31/2001

TIME: 11:38:09

Input Set : A:\227274078.ST25.txt

Output Set: N:\CRF3\08312001\I674035.raw

Application Serial Number: US/09/674,035

Alpha or Numeric: Numeric

Application Class:

Application File Date: 11-11-1999

Art Unit: PCT

Software Application: PatentIn

Total Number of Sequences: 10

Total Nucleotides: 2696

Total Amino Acids: 844

Number of Errors: 0

Number of Warnings: 0

Number of Corrections: 0

**MESSAGE SUMMARY**